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## SEQUENCE LISTING

<110> Lok, Si  
Conklin, Darrell C.  
Lofton-Day, Catherine E.

<120> Antibodies That Bind Testis-Specific  
Insulin Homolog Polypeptides

<130> 96-06C3

<140> 09/617,389

<141> 2000-07-17

<150> 09/339,148

<151> 1999-06-24

<150> 08/905,267

<151> 1997-01-18

<150> 60/023,213

<151> 1996-02-08

<150> 60/031,592

<151> 1996-11-21

<160> 24

<170> FastSEQ for Windows Version 3.0

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<211> 566

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

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1 5 10 15

gct cct ttc tcc cag gaa caa gaa gag gtc acc agc ccc acg aag ttg 96  
Ala Pro Phe Ser Gln Glu Gln Glu Val Thr Ser Pro Thr Lys Leu  
20 25 30

tgc ggc agg gac ctg ttg gta gaa gtt ata aaa ctc tgt ggc caa aat 144  
Cys Gly Arg Asp Leu Leu Val Glu Val Ile Lys Leu Cys Gly Gln Asn  
35 40 45

gac tgg agc cgg ttc tcg atg gaa gag caa agt cct atg aca gag ttg 192  
Asp Trp Ser Arg Phe Ser Met Glu Glu Gln Ser Pro Met Thr Glu Leu  
50 55 60

gtt ccc caa tat aca cgg aaa gtc aaa acc ttc aac cct cac cgg tcc 240  
Val Pro Gln Tyr Thr Arg Lys Val Lys Thr Phe Asn Pro His Arg Ser  
65 70 75 80

tcc tcc tcc tgg gga aga ttc aca aac cca ggc gtc tcc cag aag aaa 288  
Ser Ser Ser Trp Gly Arg Phe Thr Asn Pro Gly Val Ser Gln Lys Lys  
85 90 95

gca aca cac act tgg gaa tct cag tca ctg ccc aac tat cag ctt aaa 336  
Ala Thr His Thr Trp Glu Ser Gln Ser Leu Pro Asn Tyr Gln Leu Lys  
100 105 110

aag gag gag ctg ctt ccg aag aca gga gtg cat tca tac cac ggt ggc 384  
Lys Glu Glu Leu Leu Pro Lys Thr Gly Val His Ser Tyr His Gly Gly  
115 120 125

aag ccc tat gtg aag agt gta aaa ttt cag aag aaa aac act gac aaa 432  
Lys Pro Tyr Val Lys Ser Val Lys Phe Gln Lys Lys Asn Thr Asp Lys  
130 135 140

atg agt acc ttc agc ggc tta ttt tgg ggg aac cat ccc cag agg aag 480  
Met Ser Thr Phe Ser Gly Leu Phe Trp Gly Asn His Pro Gln Arg Lys  
145 150 155 160

B3 cgc aga ggt ttc gca gat aaa tgc tgt gct ata ggg tgc tcc aaa gag 528  
Arg Arg Gly Phe Ala Asp Lys Cys Cys Ala Ile Gly Cys Ser Lys Glu  
165 170 175

gag ctg gcc gtc gca tgc ctt ccg ttt gtt gat ttt ta 566  
Glu Leu Ala Val Ala Cys Leu Pro Phe Val Asp Phe  
180 185

<210> 2  
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Cys Gly Arg Asp Leu Leu Val Glu Val Ile Lys Leu Cys Gly Gln Asn  
35 40 45  
Asp Trp Ser Arg Phe Ser Met Glu Glu Gln Ser Pro Met Thr Glu Leu  
50 55 60  
Val Pro Gln Tyr Thr Arg Lys Val Lys Thr Phe Asn Pro His Arg Ser  
65 70 75 80  
Ser Ser Ser Trp Gly Arg Phe Thr Asn Pro Gly Val Ser Gln Lys Lys  
85 90 95  
Ala Thr His Thr Trp Glu Ser Gln Ser Leu Pro Asn Tyr Gln Leu Lys  
100 105 110  
Lys Glu Glu Leu Leu Pro Lys Thr Gly Val His Ser Tyr His Gly Gly  
115 120 125  
Lys Pro Tyr Val Lys Ser Val Lys Phe Gln Lys Lys Asn Thr Asp Lys  
130 135 140

Met	Ser	Thr	Phe	Ser	Gly	Leu	Phe	Trp	Gly	Asn	His	Pro	Gln	Arg	Lys
145					150					155					160
Arg	Arg	Gly	Phe	Ala	Asp	Lys	Cys	Cys	Ala	Ile	Gly	Cys	Ser	Lys	Glu
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<212> DNA
<213> Artificial Sequence
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<220>  
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<213> Artificial Sequence
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<220>  
<223> Oligonucleotide ZC10491

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<213> Artificial Sequence
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<223> Oligonucleotide ZC10685

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<210> 8

<211> 574

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<223> Human testis EST

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gtgaaagaaa	tagaaaaact	ctgcggccat	gccaactgga	gccagttccg	tttcgaggag	180
gaaacccctt	tctcacggtt	gattgcacag	gcctcggaga	aggtcgaagc	ctacagccca	240
taccagttcg	aaagcccgcg	aaccgcttcc	ccggcccggg	gaagaggcac	aaacccagtg	300
tctacttctt	gggaagaagc	agtaaacagt	tgggaaatgc	agtcactacc	tgagtataag	360
gataaaaagg	gatattcacc	ccttggtctg	ctggagtttg	ctggaggccc	actccagatg	420
ctgtttgcct	gggtatcacc	agcagaggct	gcagaacagc	aaagattgct	gcctgttcct	480
tcctctggaa	gcttcatccc	agaggggcac	ccactagatg	ccagccagag	ctttcctgta	540
tgagtgcacat	aaggattcaa	cttcaacaga	attc			574

<210> 9

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide ZC10491

<400> 9

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26

<210> 10

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC10537

<400> 10

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35

<210> 11

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC10538

<400> 11

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<210> 12  
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 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (17) ... (658)

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gga ctc ctg ctg gtt cgg ttt tct cgt gaa ctg agc gac atc agc agt	100
Gly Leu Leu Leu Val Arg Phe Ser Arg Glu Leu Ser Asp Ile Ser Ser	
15 20 25	
gcc agg aag ctg tgc ggc agg tac ttg gtg aaa gaa ata gaa aaa ctc	148
Ala Arg Lys Leu Cys Gly Arg Tyr Leu Val Lys Glu Ile Glu Lys Leu	
30 35 40	
tgc ggc cat gcc aac tgg agc cag ttc cgt ttc gag gag gaa acc cct	196
Cys Gly His Ala Asn Trp Ser Gln Phe Arg Phe Glu Glu Glu Thr Pro	
45 50 55 60	
ttc tca cgg ttg att gca cag gcc tcg gag aag gtc gaa gcc tac agc	244
Phe Ser Arg Leu Ile Ala Gln Ala Ser Glu Lys Val Glu Ala Tyr Ser	
65 70 75	
cca tac cag ttc gaa agc ccg caa acc gct tcc ccg gcc cgg gga aga	292
Pro Tyr Gln Phe Glu Ser Pro Gln Thr Ala Ser Pro Ala Arg Gly Arg	
80 85 90	
ggc aca aac cca gtg tct act tct tgg gaa gaa gca gta aac agt tgg	340
Gly Thr Asn Pro Val Ser Thr Ser Trp Glu Glu Ala Val Asn Ser Trp	
95 100 105	
gaa atg cag tca cta cct gag tat aag gat aaa aag gga tat tca ccc	388
Glu Met Gln Ser Leu Pro Glu Tyr Lys Asp Lys Lys Gly Tyr Ser Pro	
110 115 120	
ctt ggt aag aca aga gaa ttt tct tca tca cat aat atc aat gta tat	436
Leu Gly Lys Thr Arg Glu Phe Ser Ser Ser His Asn Ile Asn Val Tyr	
125 130 135 140	
att cat gag aat gca aaa ttt cag aag aaa cgt aga aac aaa att aaa	484
Ile His Glu Asn Ala Lys Phe Gln Lys Lys Arg Arg Asn Lys Ile Lys	
145 150 155	
acc tta agc aat ttg ttt tgg ggg cat cat ccc caa aga aaa cgc aga	532
Thr Leu Ser Asn Leu Phe Trp Gly His His Pro Gln Arg Lys Arg Arg	
160 165 170	
gga tat tca gaa aag tgt tgt ctt aca gga tgt aca aaa gaa gaa ctt	580
Gly Tyr Ser Glu Lys Cys Cys Leu Thr Gly Cys Thr Lys Glu Glu Leu	
175 180 185	

B3

agc att gca tgt ctt cca tat att gat ttt aaa agg cta aag gaa aaa 628  
 Ser Ile Ala Cys Leu Pro Tyr Ile Asp Phe Lys Arg Leu Lys Glu Lys  
 190 195 200

aga tca tca ctt gta act aag ata tac taa ccattcttaga atttttttcta 678  
 Arg Ser Ser Leu Val Thr Lys Ile Tyr \*  
 205 210

acctaataaaa agcttaataac atttta 703

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 <211> 213  
 <212> PRT  
 <213> Homo sapiens

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 20 25 30  
 Cys Gly Arg Tyr Leu Val Lys Glu Ile Glu Lys Leu Cys Gly His Ala  
 35 40 45  
 Asn Trp Ser Gln Phe Arg Phe Glu Glu Glu Thr Pro Phe Ser Arg Leu  
 50 55 60  
 Ile Ala Gln Ala Ser Glu Lys Val Glu Ala Tyr Ser Pro Tyr Gln Phe  
 65 70 75 80  
 Glu Ser Pro Gln Thr Ala Ser Pro Ala Arg Gly Arg Gly Thr Asn Pro  
 85 90 95  
 Val Ser Thr Ser Trp Glu Glu Ala Val Asn Ser Trp Glu Met Gln Ser  
 100 105 110  
 Leu Pro Glu Tyr Lys Asp Lys Lys Gly Tyr Ser Pro Leu Gly Lys Thr  
 115 120 125  
 Arg Glu Phe Ser Ser Ser His Asn Ile Asn Val Tyr Ile His Glu Asn  
 130 135 140  
 Ala Lys Phe Gln Lys Lys Arg Arg Asn Lys Ile Lys Thr Leu Ser Asn  
 145 150 155 160  
 Leu Phe Trp Gly His His Pro Gln Arg Lys Arg Arg Gly Tyr Ser Glu  
 165 170 175  
 Lys Cys Cys Leu Thr Gly Cys Thr Lys Glu Glu Leu Ser Ile Ala Cys  
 180 185 190  
 Leu Pro Tyr Ile Asp Phe Lys Arg Leu Lys Glu Lys Arg Ser Ser Leu  
 195 200 205  
 Val Thr Lys Ile Tyr  
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<210> 14  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Rat PC4 5' primer.

<400> 14  
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28

<210> 15  
 <211> 28

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Rat PC4 3' primer.

<400> 15  
ggaattctgt ggtctgacct cttgtctg

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<210> 16  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Motif.

<221> VARIANT  
<222> (0)...(0)  
<223> Xaa is any amino acid residue except cysteine.

<400> 16  
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<210> 17  
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<221> VARIANT  
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<223> Xaa is any amino acid residue except cysteine.

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<211> 127  
<212> PRT  
<213> Human

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Val Asp Ala Leu Gln Phe Val Cys Gly Asp Arg Gly Phe Tyr Phe Asn  
35 40 45  
Lys Pro Thr Gly Tyr Gly Ser Ser Ser Arg Arg Ala Pro Gln Thr Gly  
50 55 60  
Ile Val Asp Glu Cys Cys Phe Arg Ser Cys Asp Leu Arg Arg Leu Glu  
65 70 75 80

B3

Met Tyr Cys Ala Pro Leu Lys Pro Ala Lys Ser Ala Arg Ser Val Arg  
                     85                    90                    95  
 Ala Gln Arg His Thr Asp Met Pro Lys Thr Gln Lys Glu Val His Leu  
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 Lys Asn Ala Ser Arg Gly Ser Ala Gly Asn Lys Asn Tyr Arg Met  
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<210> 19  
 <211> 180  
 <212> PRT  
 <213> Human

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                     20                    25                    30  
 Cys Gly Gly Glu Leu Val Asp Thr Leu Gln Phe Val Cys Gly Asp Arg  
                     35                    40                    45  
 Gly Phe Tyr Phe Ser Arg Pro Ala Ser Arg Val Ser Arg Arg Ser Arg  
                     50                    55                    60  
 Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu Ala Leu Leu  
 65                    70                    75                    80  
 Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp Val Ser Thr  
                     85                    90                    95  
 Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro Val Gly Lys  
                     100                    105                    110  
 Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg Leu Arg Arg  
                     115                    120                    125  
 Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val Leu Ala Lys  
                     130                    135                    140  
 Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro Leu Ile Ala  
 145                    150                    155                    160  
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 Ser Asn Arg Lys  
                     180

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 <212> PRT  
 <213> Human

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                     20                    25                    30  
 Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe  
                     35                    40                    45  
 Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly  
                     50                    55                    60  
 Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu  
 65                    70                    75                    80  
 Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys  
                     85                    90                    95



Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn  
 100 105 110

<210> 21  
 <211> 185  
 <212> PRT  
 <213> Human

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 20 25 30  
 Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile Cys Gly  
 35 40 45  
 Met Ser Thr Trp Ser Lys Arg Ser Leu Ser Gln Glu Asp Ala Pro Gln  
 50 55 60  
 Thr Pro Arg Pro Val Ala Glu Ile Val Pro Ser Phe Ile Asn Lys Asp  
 65 70 75 80  
 Thr Glu Thr Ile Asn Met Met Ser Glu Phe Val Ala Asn Leu Pro Gln  
 85 90 95  
 Glu Leu Lys Leu Thr Leu Ser Glu Met Gln Pro Ala Leu Pro Gln Leu  
 100 105 110  
 Gln Gln His Val Pro Val Leu Lys Asp Ser Ser Leu Leu Phe Glu Glu  
 115 120 125  
 Phe Lys Lys Leu Ile Arg Asn Arg Gln Ser Glu Ala Ala Asp Ser Ser  
 130 135 140  
 Pro Ser Glu Leu Lys Tyr Leu Gly Leu Asp Thr His Ser Arg Lys Lys  
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 Arg Gln Leu Tyr Ser Ala Leu Ala Asn Lys Cys Cys His Val Gly Cys  
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 Thr Lys Arg Ser Leu Ala Arg Phe Cys  
 180 185

<210> 22  
 <211> 185  
 <212> PRT  
 <213> Human

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 20 25 30  
 Lys Leu Cys Gly Arg Glu Leu Val Arg Ala Gln Ile Ala Ile Cys Gly  
 35 40 45  
 Met Ser Thr Trp Ser Lys Arg Ser Leu Ser Gln Glu Asp Ala Pro Gln  
 50 55 60  
 Thr Pro Arg Pro Val Ala Glu Ile Val Pro Ser Phe Ile Asn Lys Asp  
 65 70 75 80  
 Thr Glu Thr Ile Ile Ile Met Leu Glu Phe Ile Ala Asn Leu Pro Pro  
 85 90 95  
 Glu Leu Lys Ala Ala Leu Ser Glu Arg Gln Pro Ser Leu Pro Glu Leu  
 100 105 110  
 Gln Gln Tyr Val Pro Ala Leu Lys Asp Ser Asn Leu Ser Phe Glu Glu  
 115 120 125

Phe Lys Lys Leu Ile Arg Asn Arg Gln Ser Glu Ala Ala Asp Ser Asn  
 130 135 140  
 Pro Ser Glu Leu Lys Tyr Leu Gly Leu Asp Thr His Ser Gln Lys Lys  
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 Thr Lys Arg Ser Leu Ala Lys Tyr Cys  
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<210> 23  
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 <212> PRT  
 <213> Human

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 Leu Cys Gly His His Phe Val Arg Ala Leu Val Arg Val Cys Gly Gly  
 35 40 45  
 Pro Arg Trp Ser Thr Glu Ala Arg Arg Pro Ala Ala Gly Gly Asp Leu  
 50 55 60  
 Pro Gln Thr Ser His His His Arg His His Arg Ala Ala Ala Thr Asn  
 65 70 75 80  
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 <211> 139  
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 20 25 30  
 Pro Arg Phe Gly Lys His Leu Leu Ser Tyr Cys Pro Met Pro Glu Lys  
 35 40 45  
 Thr Phe Thr Thr Thr Pro Gly Gly Trp Leu Leu Glu Ser Gly Arg Pro  
 50 55 60  
 Lys Glu Met Val Ser Thr Ser Asn Asn Lys Asp Gly Gln Ala Leu Gly  
 65 70 75 80  
 Thr Thr Ser Glu Phe Ile Pro Asn Leu Ser Pro Glu Leu Lys Lys Pro  
 85 90 95  
 Leu Ser Glu Gly Gln Pro Ser Leu Lys Lys Ile Ile Leu Ser Arg Lys  
 100 105 110  
 Lys Arg Ser Gly Arg His Arg Phe Asp Pro Phe Cys Cys Glu Val Ile  
 115 120 125  
 Cys Asp Asp Gly Thr Ser Val Lys Leu Cys Thr  
 130 135